

SEQUENCE LISTING

- <110> National Institute of Advanced Industrial Science and Technology
 Fujirebio Incorporated
- <120> GLYCOSYLTRANSFERASE, NUCLEIC ACID ENCODING THE GLYCOSYLTRANSFERASE AND METHOD OF TESTING CANCERATION USING THE NUCLEIC ACID

<130> YCT-902

<160> 20

<210> 1

<211> 1194

<212> DNA

<213 Homo sapiens

<400> 1

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titigticitic gagcicagga cgatgccttt giacacacce cigcccigci ggcicaccig 780 cggcccigc caccigcite ggcccgaage cictaccigg gigaggiciti tacccaggee 840 atgcctctce ggaagccagg aggaccctte tatgtgcccg agtccttctt cgaaggigge 900 tacccagcct atgcaagcgg gggtggctae gicattgccg ggcgccigge accctiggetg 960 cigcgggcgg cagcccgitit ggcaccctite ccctitigagg acgictacae tggcctitite 1020 atccgagcce tgggcciggt gccccaggee cacccagget tcctcacage ciggccagca 1080 gaccgcactig cggaccactig tgctttccge aacctgctge tggtacggee cctggc cctggccce 1140 caggccagca ttcggctctg gaaacaactig caagacccaa ggctccagtig ctga 1194

<210> 2

<211> 397

<212> PRT

<213 Homo sapiens

<400> 2

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Thr	Asp	Val	Pro	Tyr	Leu	Leu	Leu	Ala	Val	Lys	Ser	Glu	Pro	Gly	Arg
145					150					155					160
Phe	Ala	Glu	Arg	Gln	Ala	Val	Arg	Glu	Thr	Trp	Gly	Ser	Pro	Ala	Pro
				165					170					175	
Gly	Ile	Arg	Leu	Leu	Phe	Leu	Leu	Gly	Ser	Pro	Val	Gly	Glu	Ala	Gly
			180					185					190		
Pro	Asp	Leu	Asp	Ser	Leu	Val	Ala	Trp	Glu	Ser	Arg	Arg	Tyr	Ser	Asp
		195					200					205			
Leu	Leu	Leu	Trp	Asp	Phe	Leu	Asp	Val	Pro	Phe	Asn	Gln	Thr	Leu	Lys
	210					215					220				•
Asp	Leu	Leu	Leu	Leu	Ala	Trp	Leu	Gly	Arg	His	Cys	Pro	Thr	Val	
225					230					235					240
Phe	Val	Leu	Arg	Ala	Gln	Asp	Asp	Ala	Phe	Val	His	Thr	Pro	Ala	Leu
				245					250					255	
Leu	Ala	His		Arg	Ala	Leu	Pro		Ala	Ser	Ala	Arg		Leu	Tyr
			260					265	_			_	270		
Leu	Gly		Val	Phe	Thr	Gln		Met	Pro	Leu	Arg		Pro	Gly	Gly
		275		_		_	280			.	.	285			_
Pro		Tyr	Val	Pro	Glu		Phe	Phe	Glu	Gly		Tyr	Pro	Ala	Tyr
	290	0.1	0.1	0.1		295		4.1	0.1	A	300	41.	D		T
	Ser	Gly	Gly	Gly	Tyr	vaı	11e	Ala	Gly		Leu	Ala	Pro	Irp	
305					310	17 1	41.	n	Di	315	D1	C1	A	W - 1	320
Leu	Arg	Ala	Ala		Arg	vaı	Ala	PTO		Pro	Pne	GIU	ASP		ıyr
m1	0.1	T	0 -	325	A	A 1 -	T	C1	330	W- 1	D., .	C1	41.	335	Des
ınr	ыу	Leu		116	Arg	ага	Leu		ren	val	rr0	GIN		nis	r10
C1 -	DI	T	340	A 1 -	Т	D = -	A 1 ~	345	۸ ~	ጥե -	A 1 ~	۸	350	C***	A 1 a
ыy	rne	ьeu	ınr	AIA	Trp	r10	A I a	ASP	Αľg	1111	AId	иsb	піЅ	C y S	иıq

 Phe
 Arg
 Asn
 Leu
 Leu
 Leu
 Val
 Arg
 Pro
 Leu
 Gly
 Pro
 Gln
 Ala
 Ser
 Ile

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 375
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 Leu
 Gln
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 385
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 395
 397

<210> 3

<211>

<212> DNA

<213> Artificial Sequence

<220> 31

<223> Description of Artificial Sequence: 5' primer for PCR

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<210> 4

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<220> 31

<223> Description of Artificial Sequence: 3' primer for PCR

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<211> 20 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: 5' primer for RT-PCR **<400> 5** gctgttggcc gtcaagtcag 20 <210> 6 <211> 18 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: 3' primer for RT-PCR <400> 6 18 caggaagagc agccggat <210> 7 <211> 18 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: probe for RT-PCR **<400>** 7

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<211> 29	
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<211> 29	
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gccaagctta aggcctaccc cagccctcg	29
<210> 10	
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<223 Description of Artificial Sequence: 3' primer for PCR
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<211> 372

<212> PRT

<213 Homo sapiens

<400> 16

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Leu Ser Thr Arg Leu Gly Gln Thr Ile Pro Leu Pro Phe Ala Tyr Trp
35 40 45

Asn Gln Gln Trp Arg Leu Gly Ser Leu Pro Ser Gly Asp Ser Thr
50 55 60

Glu Thr Gly Gly Cys Gln Ala Trp Gly Ala Ala Ala Ala Thr Glu Ile
65 70 75 80

Pro Asp Phe Ala Ser Tyr Pro Lys Asp Leu Arg Arg Phe Leu Leu Ser 85 90 95

Ala Ala Cys Arg Ser Phe Pro Gln Trp Leu Pro Gly Gly Gly Ser 100 105 110

Gln Val Ser Ser Cys Ser Asp Thr Asp Val Pro Tyr Leu Leu Leu Ala 115 120 125

Val Lys Ser Glu Pro Gly Arg Phe Ala Glu Arg Gln Ala Val Arg Glu 130 135 140

Thr Trp Gly Ser Pro Ala Pro Gly Ile Arg Leu Leu Phe Leu Leu Gly

145 150 155 160

Ser Pro Val Gly Glu Ala Gly Pro Asp Leu Asp Ser Leu Val Ala Trp 165 170 175

Glu Ser Arg Arg Tyr Ser Asp Leu Leu Leu Trp Asp Phe Leu Asp Val

			180					185					190		
Pro	Phe	Asn	Gln	Thr	Leu	Lys	Asp	Leu	Leu	Leu	Leu	Ala	Trp	Leu	Gly
		195					200					205			
Arg	His	Cys	Pro	Thr	Val	Ser	Phe	Val	Leu	Arg	Ala	Gln	Asp	Asp	Ala
	210					215					220				
Phe	Val	His	Thr	Pro	Ala	Leu	Leu	Ala	His	Leu	Arg	Ala	Leu	Pro	Pro
225					230					235					240
Ala	Ser	Ala	Arg	Ser	Leu	Tyr	Leu	Gly	Glu	Val	Phe	Thr	Gln	Ala	Met
				245					250					255	
Pro	Leu	Arg	Lys	Pro	Gly	Gly	Pro	Phe	Tyr	Val	Pro	Glu	Ser	Phe	Phe
			260					265					270		
Glu	Gly	Gly	Tyr	Pro	Ala	Tyr	Ala	Ser	Gly	Gly	Gly	Tyr	Val	Ile	Ala
		275					280					285			
Gly	Arg	Leu	Ala	Pro	Trp	Leu	Leu	Arg	Ala	Ala	Ala	Arg	Val	Ala	Pro
	290					295					300				
Phe	Pro	Phe	Glu	Asp	Val	Tyr	Thr	Gly	Leu	Cys	Ile	Arg	Ala	Leu	Gly
305					310					315					320
Leu	Val	Pro	Gln	Ala	His	Pro	Gly	Phe	Leu	Thr	Ala	Trp	Pro	Ala	Asp
				325					330					335	
Arg	Thr	Ala	Asp	His	Cys	Ala	Phe	Arg	Asn	Leu	Leu	Leu	Val	Arg	Pro
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Leu	Gly	Pro	Gln	Ala	Ser	Ile	Arg	Leu	Trp	Lys	Gln	Leu	Gln	Asp	Pro
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3	370	3′	72												

<210> 17

<211> 282

<212> PRT

<213> Homo sapiens

<400	> 17														
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Pro	Tyr	Leu	Leu	Leu	Ala	Val	Lys	Ser	Glu	Pro	Gly	Arg	Phe	Ala	Glu
		35					40					45			
Arg	Gln	Ala	Val	Arg	Glu	Thr	Trp	Gly	Ser	Pro	Ala	Pro	Gly	Ile	Arg
	50					55					60				
Leu	Leu	Phe	Leu	Leu	Gly	Ser	Pro	Val	Gly	Glu	Ala	Gly	Pro	Asp	Leu
65					70					75					80
Asp	Ser	Leu	Val	Ala	Trp	Glu	Ser	Arg	Arg	·Tyr	Ser	Asp	Leu	Leu	Leu
				85				÷	90					95	
Trp	Asp	Phe	Leu	Asp	Val	Pro	Phe	Asn	Gln	Thr	Leu	Lys	Asp	Leu	Leu
-			100					105					110		
Leu	Leu	Ala	Trp	Leu	Gly	Arg	His	Cys	Pro	Thr	Val	Ser	Phe	Val	Leu
	1	115				1	120					125			
Arg	Ala	Gln	Asp	Asp	Ala	Phe	Val	His	Thr	Pro	Ala	Leu	Leu	Ala	His
	130					135					140				
Leu	Arg	Ala	Leu	Pro	Pro	Ala	Ser	Ala	Arg	Ser	Leu	Tyr	Leu	Gly	Glu
145					150					155					160
Val	Phe	Thr	Gln	Ala	Met	Pro	Leu	Arg	Lys	Pro	Gly	Gly	Pro	Phe	Tyr
				165					170					175	
Val	Pro	Glu	Ser	Phe	Phe	Glu	Gly	Gly	Tyr	Pro	Ala	Tyr	Ala	Ser	Gly
			180					185				•	190		
Gly	Gly	Tyr	Val	Ile	Ala	Gly	Arg	Leu	Ala	Pro	Trp	Leu	Leu	Arg	Ala
		195					200					205			
Ala	Ala	Arg	Val	Ala	Pro	Phe	Pro	Phe	Glu	Asp	Val	Tyr	Thr	Gly	Leu
	210					215					220				

Cys Ile Arg Ala Leu Gly Leu Val Pro Gln Ala His Pro Gly Phe Leu 225 230 235 240 Thr Ala Trp Pro Ala Asp Arg Thr Ala Asp His Cys Ala Phe Arg Asn 245 250 Leu Leu Leu Val Arg Pro Leu Gly Pro Gln Ala Ser Ile Arg Leu Trp 260 265 270 Lys Gln Leu Gln Asp Pro Arg Leu Gln Cys 275 280 282

<210> 18

<211> 1845

<212> DNA

<213> Mouse

<400> 18

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ccagcigcic igaiaaggai giaccciaci igciaciggo igicaaaica gaaccaggac 960 actitigcage acggeagget gigagggaga cetggggeag eccagitiget gggaceeggt 1020 tgctcttcct gctggggtcc cccctaggaa tgggggggcc tgacttaaga tcactggtga 1080 cgtgggaaag ccggcgctat ggtgacctac tgctctggga cttcctggat gttccctaca 1140 accggacact caaggacctg ctgctgctga cctggctgag ccaccactgc cccgatgtca 1200 attitigicot geaggiteag gaigaigeet tigigeaeat eccageeeta eiggageaee 1260 tgcagactct gccacccacc tgggcccgca gcctctacct gggtgagatc ttcacccagg 1320 ccaaaccgct ccgcaagccc ggaggaccct tctatgtgcc gaagaccttc tttgaagggg 1380 actatccage ctatgcgagt ggaggtgget atgtaatete aggacgcetg geaccetgge 1440 tgctgcaggc ggcagctcgc gtggcaccct tcccctttga tgatgtctac actggcttct 1500 gcttccgtgc cctgggctta gcaccccgtg cccatccagg cttcctcaca gcctggccag 1560 cagaacgtac cagggacccc tgcgccgtgc gaggcctgct cttggtgcat ccagtcagcc 1620 ctcaggacac catttggctc tggagacatc tgtgggtccc agagctccag tgctgaccgg 1680 cagagacaag ctggggtggg tgggtgctga cctggcctga gtctctccta gagacaagct 1740 ggggtgggtg gggctgacct ggcctgagtc tctcctaaac ccttcttagc caaggtggca 1800 1845 gactgtgttt atctacttta tggttttgaa aaatgtgtcc ttcct

<210> 19

<211> 1170

<212> DNA

<213> Mouse

<400> 19

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tactigctac tegetgicaa atcagaacca ggacactite cagcacgca ggctegagg 480 gagacctegg gcagcccagt tectgegacc cegitectci tectgetegg gtccccccta 540 ggaategggg gccteacti aagatcacte gtgaceggg aaagcceggc ctateggtgac 600 ctactectct gggacticct ggateticcc tacaaccgga cactcaagga cctectegeteg 660 ctgacctegc teagccacca cigccccgat gtcaattite tectgcagg tcaggategat 720 gcctttete acateccage cctactegag cacctegaga ctctecacc caccteggcc 780 cgcagcctct accteggta gateticacc caggccaaac cgctcegcaa gcccggagga 840 cccttctate tectgagacc cttetitgaa ggggactatc cagcctate gagtggaggt 900 ggctatetaa tctcaggace cctegcacc tegetgece tegetgec tegetgece 1020 cgtgcccatc caggctict cacactege ccacactege cacactege cttagcaccc 1020 cgtgcccatc tegettee tegetgete agccctcagg acaccattee gctctggaga 1140 catctegtgg tcccaggct tccagagct ccagtegta

<210> 20

<211> 389

<212> PRT

<213> Mouse

<400> ⋅ 20

Glu Pro Thr Leu Pro Thr Asn Leu Ser Ala Arg Leu Gly Gln Thr Gly
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Pro Leu Ser Ser Ala Tyr Trp Asn Gln Gln Gln Arg Gln Leu Gly Val 65 70 75 80

Leu	Pro	Ser	Thr	Asp	Cys	Gln	Thr	Trp	Gly	Thr	Val	Ala	Ala	Ser	Glu
				85					90					95	
Ile	Leu	Asp	Phe	Ile	Leu	Tyr	Pro	Gln	Glu	Leu	Arg	Arg	Phe	Leu	Leu
			100					105					110		
Ser	Ala	Ala	Cys	Arg	Ser	Phe	Pro	Leu	Trp	Leu	Pro	Ala	Gly	Glu	Gly
	1	115				1	120					125			
Ser	Pro	Val	Ala	Ser	Cys	Ser	Asp	Lys	Asp	Val	Pro	Tyr	Leu	Leu	Leu
	130					135					140				
Ala	Val	Lys	Ser	Glu	Pro	Gly	His	Phe	Ala	Ala	Arg	Gln	Ala	Val	Arg
145					150					155					160
Glu	Thr	Trp	Gly	Ser	Pro	Val	Ala	Gly	Thr	Arg	Leu	Leu	Phe	Leu	Leu
				165					170					175	
Gly	Ser	Pro	Leu	Gly	Met	Gly	Gly	Pro	Asp	Leu	Arg	Ser	Leu	Val	Thr
			180					185					190		
Trp	Glu	Ser	Arg	Arg	Tyr	Gly	Asp	Leu	Leu	Leu	Trp	Asp	Phe	Leu	Asp
		195					200					205			
Val	Pro	Tyr	Asn	Arg	Thr	Leu	Lys	Asp	Leu	Leu	Leu	Leu	Thr	Trp	Leu
	210					215					220				
Ser	His	His	Cys	Pro	Asp	Val	Asn	Phe	Val	Leu	Gln	Val	Gln	Asp	Asp
225					230					235					240
Ala	Phe	Val	His	Ile	Pro	Ala	Leu	Leu	Glu	His	Leu	Gln	Thr	Leu	Pro
				245					250					255	
Pro	Thr	Trp	Ala	Arg	Ser	Leu	Tyr	Leu	Gly	Glu	Ile	Phe	Thr	Gln	Ala
			260					265	•				270		
Lys	Pro	Leu	Arg	Lys	Pro	Glý	Gly	Pro	Phe	Tyr	Val	Pro	Lys	.Thr	Phe
		275					280					285			
Phe	Glu	Gly	Asp	Tyr	Pro	Ala	Tyr	Ala	Ser	Gly	Gly	Gly	Tyr	Val	Ile
	290					295					300				
Ser	Gly	Arg	Leu	Ala	Pro	Trp	Leu	Leu	Gln	Ala	Ala	Ala	Arg	Val	Ala
305					310					315					320

Pro Phe Pro Phe Asp Asp Val Tyr Thr Gly Phe Cys Phe Arg Ala Leu Gly Leu Ala Pro Arg Ala His Pro Gly Phe Leu Thr Ala Trp Pro Ala Glu Arg Thr Arg Asp Pro Cys Ala Val Arg Gly Leu Leu Val His Pro Val Ser Pro Gln Asp Thr Ile Trp Leu Trp Arg His Leu Trp Val Pro Glu Leu Gln Cys